

1 CCATTCAAA CAAGTCAGGA AAGCCTGCAC AGGACTGGAT AAATAATTAA
51 GAAACAGAGTG TTCTGAACAT CAACACAAAC TGGAAAGAACCC TTAAGCTGAA
101 GGTACAGTAT ATTATTTACA CTGAAGGGC TTCTGTGTGG ACAAGGAAAGC
151 GGTGACAGCT CAAATGGATC CCATGGAACG GAGAAATGTC AACATCGAAC
201 GAGATGATGA GAGCAGCAGT GGAAAGAAAGC CTGGAGATAG CTACATCAGG
251 ATAGGAATT CAGAAAAGGC AGCAATGACC AGTCGAAATTG CTAATGAAAG
301 CACTGAAAGT CAGAAATTCG TGACTAAAGG ATTTTGAGGG AAAAAAGAAC
351 TGCGAGATTA TGCTGATGAA CACCATCGG GAGGCACTTC CTTTGGAAATG
401 TCTTCATTTA ACCTGAGTAA TGGCATCATG CCGAGTGGGA CCCTGGGCTT
451 GGTCTATGCC ATGGCCTACA CAGGGGTAT ATTTTTATAA ATCATGCTGC
501 TTCTGTGGC AATATTATCA CTGTATTCAAG TTGACCTTT ATTAAAAAAC
551 GGTAAAGCAAG GAGGGTCTTT GATTATGAA AAATTAGGAG AAAAGGCATT
601 TGGATGCCCG GGAAAATGG GAGCTTTCTG TGGATTACAA ATGCAGAAC
651 TTGGAGCAAT GTCAGCTAC CTCTTATCA TAAATATGA ACTACCTGAA
701 GTAATCAGAG CATTGATGGG ACTTGAAGAA AATACTGGAG AATGGTACCT
751 CAATGGCAAC TACCTCATCA TATTGTTGTT TGGTGGAAATT ATTCTTCAC
801 TTTCGCTCT TAAAAATTTA GGTTATCTG GGTATACACAG TGGATTTTCT
851 CTTACCTGCA TGGTGTGTT TGGTAGTGCG GGTGTTACAA AGAAATTCCA
901 AATACCTGCG CCTCTACCTG TTTGGATCA CAGTGGTSGA AATCTGTCA
951 TCAACAACAC GCTTCCAATG CATGGGTAAGT GTTACCCAA CAACTCTGAG
1001 AGTTCTGATG TGAACCTCAT GATGGATTAC ACCACACCGCA ATCCTGCAGG
1051 GGTGGATGAG AACCAAGGCCA AGGGCTCTG TGTGACAGT GGAGTAGAAAT
1101 ATGAAGCTCA TAGTGATGAC AAGTGTGAA CAAATACCTT TGTATTCAAC
1151 TCCCGGACCG CCTATGCAAT TCTTATGCA GTATTTGCTT TTGTATGCCA
1201 CCCTGAGGTC CTTCCCATCT ACAGTGAACG TAAAGATCGG TCCCGGAGAA
1251 AAATGCAAC CCGTCAAAT ATTCCATCA CGGGGATGCT TGTATGTAC
1301 CTGCTTGCGG CCCTTGTGG TTACCTAACG TTCTATGGAG AAGTIGAAGA
1351 TGAATTACTT CATGCTACA GCAAAGTGTAA TACATTAGAC ATCCCTCTTC
1401 TCAATGGTCC CCTCCCCATC CTCTCTCTT TAAACAAAC TGTGCCCCATT
1451 GTCCTCTTCC CAATTGTCAC ATCAGTGATG ACACGTGTTAT TTCCCAAACG
1501 ACCCTTCAGC TGGATACGAC ATTCCCTCAT TGCAGCTGTG CTTATTGCCAC
1551 TTAATAATGTTCTGGTCATC CTGTCGCGAA CTATAAAATA CATCTTCGGA
1601 TTCATAGGGG CTTCTCTGC CACTATGTC ATTTTTATTC TTCCAGCAGT
1651 TTTTTATCTT AAACCTGTCA AGAAAGAAC TTTTAGGTCA CCCCAAAGG
1701 TCGGGGTTT AATTTCCCTT GTGGTTGGAA TATTCTTCAT GATTGGAAAGC
1751 ATGGCACTCA TTATAATTGA CTGGATTAT GATCCTCCAA ATTCCAAGCA
1801 TCACTAACAC AAGGAAAAAT AC

FEATURES:

5'UTR: 1-163
Start Codon: 164
Stop Codon: 1805
3'UTR: 1808

HOMOLOGOUS PROTEINS:

Top BLAST Hits:

		Score	E
CFA 145000003337444	/altid=gi 12017941 /def=gb AAG45335.1 AF295...	975	0.0
CFA 1140000033649823	/altid=gi 10945621 /def=gb AAG24618.1 AF293...	597	e-169
CFA 160000003782430	/altid=gi 18677401 /def=gb AAF75589.2 AF1736...	591	e-168
CFA 143000002720069	/altid=gi 18248427 /def=gb AAF74195.1 AF2495...	587	e-166
CFA 87000000006802	/altid=gi 7243145 /def=dbj BAA92620.1 (AB03...	573	e-164
CFA 180000005069115	/altid=gi 5870493 /def=ref NP_006832.1 tran...	500	e-140
CFA 890000001154721	/altid=gi 7406150 /def=gb AAF61849.1 AF15985...	496	e-139
CFA 65000019404613	/altid=gi 9506137 /def=ref NP_061849.1 amin...	495	e-139
CFA 100000004435450	/altid=gi 8906332 /def=gb AAF81797.1 AF2730...	492	e-138
CFA 335001093689635	/altid=gi 11444147 /def=ref XP_006635.1 hy...	480	e-134

EST:

gi 10934204	/dataset=dbest /taxon=96...	1072	0.0
gi 10286121	/dataset=dbest /taxon=96...	718	0.0
gi 9872634	/dataset=dbest /taxon=960...	680	0.0
gi 2616674	/dataset=dbest /taxon=9606 ...	549	e-154
gi 9882497	/dataset=dbest /taxon=960...	541	e-151
gi 689641	/dataset=dbest /taxon=9606 /...	525	e-147

EXPRESSION INFORMATION FOR MODULATORY USE:

library source:

Expression information from BLAST dbEST hits:

gi|10934204 Whole embryo (mainly head)
gi|10286121 Hepatocellular carcinoma
gi|9872634 Non-cancerous liver
gi|2616674 retai liver spleen
gi|9882497 Non cancerous liver
gi|689641 Liver

Expression information from PCR-based tissue screening panels:

Mixed tissue (Brain, Heart, Kidney, Lung, Spleen, Testis, Leukocyte)

1 MDPMEPLNVN IEPDDESSSG ESAPDSYIRI GNSEKAAMSS QFANEIDTESQ
51 KFLTNFLGK PKLADYADEH HPGTTSGMS SFNLNSNAIMG SGILGLSYAM
101 AYTGVILFII MLLAVAILSL YSVHLLKTA KEGGSLIYEK LGEKAFGWPG
151 KIGAFVSGTM QNIGAMSSYL FIIKYLEPEV IRAFTMGLEEN TGEWYINGNY
201 LCLIFVSGVGI LPLSLLKNLG YLGYTSGFSL TCMVFFVSVV IYKEFQIPCP
251 LPVLIPLGVGH LCFNNTLPMH VVMLPNSES SDVNFMMMDYT HRNPAGLDEN
301 QAKGSLRDSG VEYEAHSDDK CEPKHFVFNS FTAYAIPILV FAFVCHPEVL
351 FLYSEFIFDRM PRKMQTVSNI SITGMLVMYL IAAALFGYLTF YGEVEEELLH
401 AYSKVVTTLDI PLLMVRALV VAVTQTVPIV LFPIFTSVIT LLFPKRPFSW
451 IRRHFLIAAVL IALNNVLVIL VPTIIFYIFGF IGASSATMLI FILPAVFYLK
501 LVKKEFESPF QKVGALIFLV VGIFFMIGSM ALIIDWIYD PPNSKHH

FEATURES:

Functional domains and key regions:

[1] PI_C00001 PS00001 ASN_GLYCOSYLATION
N-glycosylation site

Number of matches: 5

1	83-86	NLSN
2	160-163	NLSF
3	264-267	NNTL
4	276-279	NNSE
5	369-372	NISI

[2] PDC00004 PS00004 CAMP_PHOSPHO_SITE
cAMP- and cGMP-dependent protein kinase phosphorylation site

133 503 KNET

[3] PDC00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

Number of matches: 7

1	33-35	SEK
2	49-51	SQK
3	129-131	TAK
4	290-292	THR
5	360-362	SRR
6	473-475	TIK
7	506-508	TFR

[4] PDC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 5

1	18-21	SSGE
2	22-25	SAPD
3	129-132	TAKE
4	305-308	SLHD
5	309-312	SGVE

[5] PDO00008 PS00008 MYPISTYL
N-myristoylation site

Number of matches: 6

1	95-100	GLSYAM
2	153-158	GAFVSI
3	164-169	GAMSSY
4	186-191	GLEENT
5	296-301	GLDENQ
6	482-487	GASSAT

[6] PDO00009 PS00009 AMIDATION
Amidation site

58-61 LGKK

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	79	99	1.125	Certain
2	102	122	2.503	Certain
3	153	173	1.197	Certain
4	197	217	1.785	Certain
5	222	242	2.123	Certain
6	332	352	1.240	Certain
7	370	390	2.166	Certain
8	414	434	1.301	Certain
9	453	473	1.520	Certain
10	476	496	2.166	Certain
11	515	535	2.628	Certain

BLAST Alignment to Top Hit:

>CRAI145000039337444 /altid=q:12017311
/def=gb|AAG45335.1|AF295535_1 (AF295535) amino acid
transport system A3 [Rattus norvegicus] /org=Rattus
norvegicus /taxon=10116 /dataset=nraa /length=547
Length = 547

Score = 975 bits (2492), Expect = 0.0
Identities = 478/547 (87%), Positives = 508/547 (92%)

Query: 1 MDPMELEVNIEPDESSSGESAPDSYIRIGNSEKAAMSSQFANEDETESQFFLTNGFLGH 60
MDP+ELP+VNIEP ++S S Y +GNSEK AM SQFANE ESQFFLTNGFLGH
Sbjct: 1 MDPIELFSVNIEPYEDSCNVDIQSCTGMGNSEKGAMDSQFANEDEASQFFLTNGFLGH 60

Query: 61 EFLADYADEHHPGTTSF M:SFNLNSNAIMGSGILGLSYAMAYTGVLFIIMLLAVAILSL 120
E L DYADEHHPGTTSFGM:SFNLNSNAIMGSGILGLSYAMA TG++LF+IMLL VAILSL
Sbjct: 61 ETLTDYADEHHPGTTSFGM:SFNLNSNAIMGSGILGLSYAMANTGIVLFVIMLLTVAISSL 120

Query: 131 YSVHLLLKTAKEGGSLIYFHLGEKAFGWPGKIGAFVSITMQNIGAMSSYLFIIKTELPEV 180
YSVHLLLKTAKEGGSLIYFHLGEYAFGWPGKIGAF+SITMQNIGAMSSYLFIIKTELPEV
Sbjct: 131 YSVHLLLKTAKEGGSLIYFHLGEKAFGWPGKIGAFISITMQNIGAMSSYLFIIKTELPEV 180

Query: 181 IFAFMGLEENTGEWYLN G+LII FVSVGIIPLSLLKNLGYLGYTSGFSLTCMVFFVSVV 240
IE FMGLEENTGEWYLN G+L++FVSVGIIPLSLLKNLGYLGYTSGFSLTCMVFFVSVV
Sbjct: 181 IRVFMGLEENTGEWYLN G+LIVL FVSVGIIPLSLLKNLGYLGYTSGFSLTCMVFFVSVV 240

Query: 241 IYKKFQIPCPPLPVLDHSVGNLSFNNLPMHVMLPNNSSESDVNFMMDYTHPNPAGLDEN 300
IYKKFQIPCPPLPVLDH+ GNL+FNNTLPMHV+MLPNNSES+ +NFM+DYTHP+F GLDE
Sbjct: 241 IYKKFQIPCPPLPVLDH+ GNL+FNNTLPMHV+MLPNNSES+GFM+DYTHP+F GLDE 300

Query: 301 QAKGSLHDSGVEYEAHSDDECEPKYFVFNSETAYAIPILVFAFVCHPEVLPYISELKDRS 360
A G LH SGVEYEAHSDCEPKYFVFNSETAYAIPIL FAFVCHPEVLPYISELKDRS
Sbjct: 301 PAAGPLHSGSGVEYEAHSGLKCQPKYFVFNSETAYAIPILAFAFVCHPEVLPYISELKDRS 360

Query: 361 RRKMQTVDNISITGMLVMIILAALFGYLTFYGEVEDELLHAYSKVYTLIDIPLLMVRALV 420
RRKMQTVDNISITGMLVMIILAALFGYL+FYGEVEDELLHAYSKVYD LLMVRALV
Sbjct: 361 RRKMQTVDNISITGMLVMIILAALFGYLSFYGEVEDELLHAYSKVYTFDALLMVRALV 420

Query: 421 VAVTQTVPIVLFPPISTSITLLFPKRPFWSIRHFLIAAVLIALNNVLV1LVPTIKYIFGF 480
VAVT TVPIVLFPPISTSITLLFP+RPFWS++HF IAA++IALNNVLV1LVPTIKYIFGF
Sbjct: 421 VAVTQTVPIVLFPPISTSITLLFPKRPFWSVWKHFGIAAIIIAALNNVLV1LVPTIKYIFGF 480

Query: 481 IGASSATMLIFILPAVFYLFLVKKETFRSPQKVGVGALIFLVVGIFFMIGSMALIIIDWIYD 540
IGASSATMLIFILPA FYLFVKKE RSPQK+GAL+FLV GI FM+GSMALIIIDWIY+
Sbjct: 481 IGASSATMLIFILPAFAFYLFLVKKEPLRSPQKIGALVFLVTGII FMMGSMALIIIDWIYD 540

Query: 541 PPNSKHH 547
PPN HH
Sbjct: 541 PPNPDH 547

>CRAI114000033649823 /altid=q:10945621
/def=gb|AAG24618.1|AF298897_1 (AF298897) amino acid
transporter system A [Homo sapiens] /org=Homo sapiens
/taxon=9606 /dataset=nraa /length=506
Length = 506

Score = 597 bits (1522), Expect = e-169
Identities = 315/549 (57%), Positives = 383/549 (69%), Gaps = 46/549 (8%)

Query: 1 MDPMELRNVNIEPDESSSGESAPD---SYIRIGNSEKAAMSSQFANEDETESQFFLTNGF 57
M E+ +I PD+SSS S D SY +++AA+ S +A+ D E+Q FL
Sbjct: 1 MKKAEMGRFSISPDEDSSYSSNSDFNYSY---PTKQAALKSHYADVDPENQNLLESN 56

Query: 58 LGKKHLADYADEHHPGTTSGM3SFNLNAIMGSGILGLSYAMAYTGVLFLIMLLAVAI 117
 LGKKH T E HPGTTSGM3 SFNLNAIMGSGILGLSYAMAYTGVLFLIMLLAVAI 117
 Sbjct: 57 LGKKH---TETEFHPGTTSGM3VFNLNAIVGSGILGLSYAMANTGIALFIILLTFVSI 113

 Query: 118 LSLYSVHLLLTAKEGGSLIYEELGEKAFGWPGRIGAFVSITMGNIGAMSSYLFIIKYEL 177
 SLYSVHLLLTAKEGGSLIYE+LG KAFG GK+ A SITMGNIGAMSSYLFIIKYEL
 Sbjct: 114 FSLYSVHLLLTAKEGGSLIYEQLGYKAFGLVGKLAASGSITMGNIGAMSSYLFIVKYEL 173

 Query: 178 PEVIPAFMGLEENTGEWYINGGILIFVSGIILPLSLLKNLGYLGYTSGSLLCMVFFV 237
 P VI+A +E+ TG WYLNFGPL++ VS+ +IPLSL +NLGYLGYTSG SL CMVFF+
 Sbjct: 174 PLVIQALTNIEDKTGLWYLNFGYLVLVSLVILPLSLLFRNLGYLGYTSGSLLCMVFFV 233

 Query: 238 SVVIYKKFQIPCPPLPVLDHSWGNLSPNNTLPMHVVMLPNNSESSIVNFMDYTHRNPAGL 297
 VVI YKFQ+PCP- + N + M TL ++P
 Sbjct: 234 IVVICKKFQVPCPVEAA -LQINETINTLTLQPTALVP----- 269

 Query: 298 DENQAFGSLHDSGVEYEAHSDMCEPKYFVNSRTAYAIPILVFAVCHPEVLPYSELK 357
 + + +II C P YF+FNS+T YA+PIL+F+AVCHP VLPIY ELK
 Sbjct: 270 -----ALSHNVTENDOCRPHYFIFNSQTVYAVPILIFSVCVCHPAVLPYEEELK 317

 Query: 358 DRSPRFMQTVSNISITGMLVMYLLAALFGYLTFYGEVEDELLHAYSKVYTLIDIPLLMVR 417
 DRSPRF+M VS IS M +MYLLAALFGYLTFY VE ELLH YS + DI LL+VRL
 Sbjct: 318 DRSPRFMMNVSKISFFAMFLMYLLAALFGYLTFYEHVESELLHTYSSILGTDILLIVRL 377

 Query: 418 AVLVAVTQTVPIVLFPPTSVITLLFPKPPFSWIRHFLIAAVLIALNNVLVILVPTIKYI 477
 AVL+AVT TVP+V+FPIF+SV LL + FSW RH LI ++A N+LVI VPTI+ I
 Sbjct: 378 AVLMAVTLLTVPVVIFPFSVTLLCASKDFSWWRHSLITVSILAFTNLLVIFVPTIRDI 437

 Query: 478 FGFIGASSATMLIFILPAVFYKLVLKKETFRSPQKVGALIFLVVGIFFMIGSMALIIDW 537
 FGFIGAS+A+MLIFILP+ FY+KLVKKE +S QK+GAL FL+ G+ M GSMALI++DW
 Sbjct: 438 FGFIGASAASMLIFILPSAFYIKLVKEPMKSVQKIGALFFLSGVLVMTGSMALIVLDW 497

 Query: 538 IYDPPNSKH 546
 +++ P H
 Sbjct: 498 VHNAPGGGH 506

Hmmer search results (Pfam):

Model	Description	Score	E-value	N
PF01490	Transmembrane amino acid transporter protein	187.0	2.9e-52	2
CE00398	E00398 CD53	4.0	4.8	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
CE00398	1/1	90	110	..	1 23 [. 4.0	4.8	
PF01490	1/2	99	236	..	1 179 [. 58.9	2.5e-14	
PF01490	2/2	305	529	..	200 467 .] 133.9	3e-36	

1 AGCTTAGCAA TATGGATCAA GAGGTGAAAT ACCTGATTAA TAAAAGTTTC
51 AGGAGTAAAC AAAGGTTGAG GAAATTTTT TTTAAATACT AGAACTTTT
101 TTATTTTAG AAAATTC TTTCTATAGAA GAAAGACAAG CCTTTGATT
151 GGGGCTCTG CATGCTGAA TTTGAGAATT TTTAAAGCGA CTGACATCTA
201 GTCACTCGT GATGAAAAGA TGGGATAAA AATTGTGAAA TGGTCAGAAA
251 ACCATGATA AATTATTTAT GAAATAAA GAGGAGACT GAGCAATAGA
301 AGCTAGAAGA GAGAAATTTC TTTCTATTC TGAAGGAAAA TGCTCTGAA
351 TCTAGAATTG AAACATTTAA GAAATTTGA AGGCAAAATA AAGAATTTC
401 CAACATGAG CAACTGAAAT TTTTATTTA CAGACATAGG CTGATTGTG
451 GAAAAAGTT ATTGAGA TAAATTTAGC ATAATGCAA AATAACTGAA
501 GAAAGAAGAT AGAATGGT TAAATTAATG AGCAGCTGAG CAAGACTGAG
551 AGGTTGGAGG AGGAAGGAT TAAATATGAG AAAGAGCATA GAAAATTTGC
601 TTCAAGTT TTGGAAAT AATAATATAT TTCACTTATT ATGTTAGTAA
651 ATACACACT TTGCTTGGT GAGCTACTAT TTATACAGT GATAATACGT
701 AATTGCTGCT TATTGTTT GATTTAG AAACAACTA CAGGCAACTT
751 ATGACACTTG TTTCATTTAA GAAATGAAA ATATTATGAT TTGCAATTG
801 TAAAAGTATT TTATTAATA AAATAATTAG GAGTGTAGGA CAAGGAAAGG
851 AAGAAAGAAA AAGTATGTTA AGTGTCTTAT TTGTTATGGG TAACCAGTGT
901 AAAATCAGTA AACCAAGGAA AAAAAAGTTT AGTGAATTAT TCAGATCTAG
951 AATGGCTAAC TTTAAGTAC AGTGTAAAAA CAGAAACGCT CAATAGTGGT
1001 TGCTGCTGGG AAGTGAGAA TTTAATGTGT GAAGAATGAG GAAAACCTTT
1051 CTACTCATTT AGTGAGTTTC TTGTTTTTTT CTTTACCCA TATGCACTG
1101 TTACTCTAT TCTCTCTTGT TTTTAACCT GCTTCTTTTC ATCTTTTATG
1151 TATATACATT TAGGCTGTTT GATTTAAATA ATAGTTTCAT TTTGTTCT
1201 CCTGCTTAA ACATGTTGTG GATTTTTTTT AAATTCTGAG AACTGCTTTC
1251 TTATTTCTA GACAATTGTC TGGCAATTATC TTGTTCTGTG TTGCTCTAC
1301 CTAGTCAC AATTCTAT ATGCAATGAA CTATCAGTGT ATATTGAC
1351 TTGTAATTCT TATTGTTTC GATTTCTCT TAACTTCTTA TTTGTTTTT
1401 TCTTTTTTTA ATCTCTTAT GATTTAAATT GAGTGATTC CAGAGATCTG
1451 TCTTTCAATT TTATAAGTCT TCTTCAGCT GAGTTTTTTT AAATTCAAT
1501 GATTCTATT TTTCTTTT TTAAAGAAAT CTTTTTTTG ACTCTTTTG
1551 CAACAGCTG TTCTCCTTTT ATATTCTTT ATAATGTTT TATTCTGTGA
1601 AAGTTATTCT CTTATTTGAG ATGTTTTCTT TCAAAATGTC TTTCTTTTA
1651 TTAATTAAAT GTAAAAGTTC CTTTAAATT GCTTTGTAT TTGAGTTCC
1701 TTAGATGTGA ATTATTCAT TTCTGTGCC TACTGGCACT CTTGCTAGT
1751 AGTTCCATG TGTGTTAT ATGTTTGTAA ATTGAGGAT GTGAACCTT
1801 CTCAAGTGTG AGTTGCTTT CAAAAAAGTA CTGCCATGGC ACTGGGTG
1851 GGAGGTATTG CCATGTGGTA GTTCTGTGTT GTCAGAGGAA TAGCACATT
1901 TGTGACTTCT GGAGCAATT TTATGTTAGT TTCTCTGCTC AAGATTCT
1951 TATCAATGG GTATTGACCA TGTCAATGACC ACACCTTCA AGAATGATAG
2001 TGTTCTCTT AATACGATGG TTCAACAAATA ATTGAATGAA TCTAATGGTA
2051 AGAATTTCAG AAGAAATTAT ATCAACTACA TATAGTAGAT TCAAGGATT
2101 TTCAAAAC ACAATGCCAG TCCACCCCTT TTCACATAC AATTGAGGAA
2151 AATGAGGCC CCAAATGTTA AATGACTTCT GCTGAGATCC AATGAATTA
2201 AGGCAGAGCA GAGGCTAAA TCTAGATCTC TTTGTTGTTA AAATACATT
2251 TAATTGACA CAGATGATGA GTAATGCTGA CCCAGAGGTA AATCTGAACT
2301 TTCTTTGTT ACTATCTTAA ACTTTGGCTT CAGGATCCAA GTGCTAGAA
2351 AGTTACTTCC TAAACTCTGAT CCTCACCTAT GTTGCAATTAT ATCAAGCATT
2401 TGGGGTGTGTT AATTCTTTAA TGTCCAATTAA AATTAAAGCA GTAACTTCT
2451 TTCTAGTTAT TGCTAGTAGA GACACTGGTA GATTCTGCTC TGGTAGACCT
2501 TCCTCTGCA ACAATTCTA TTTGCTCTCC TTTCTTTAA AACATGATAC
2551 CCACTCACAA ATACCTAAAT TTCCCTGAAG ACTGCTGCCA TGTTTAAGA
2601 TTTCTTTTT TTCCATAGT GACTAGTAA ACCTGCCATT TTGCTTATAC
2651 ATAGGCACTC TATAAAATATC TGCTAATTAA GCAATTATTA GTAATTCT
2701 TTCTTCTCTT CCATTCTTC TTGCTGTGTA TTGGGAAAG GAAATTC
2751 GGATTTGCTT ATGTAAGTGT TTCAAGGAGT TCTTTCTTC CTGCTTCTT
2801 CAGAGAGCAT ACAAAATGTA GATGATTGAT ATTCACTTAT TTGATTTAA
2851 TAAAATTATA ATGATGATG TTGTTGTTGTG TTTGAGAAC AGAGTGTCT
2901 GAACATCAAC ACAAAATGGA AGAACCTTAA GCTGAAGGTA CAGTATATTA
2951 TTTACACTGA AGGGCTTGT GTGTTGGACAA GAAAGGCTG ACAGCTCAA
3001 TGGATCCCAT GGAACCTGAGA AATGTCACAA TCGAACCCAGA TGATGAGAGC
3051 AGCAGTGGAG AAAGTGTTC AGATAGCTAC ATCGGGATAG GAAATTGAGA
3101 AAAGGCAGCA ATGAGCAGGT ATGGGGTTAA AAATTACTAT GTTCCATGGA

FIGURE 3, page 1 of 23

3151 AAAATAAGAC AGGATGTGGA CATGGAAAAC AGGGTTTGA TGGGAAGAAC
3201 TGGATTATT ACAGGTTAAAT TTGTTGATAAT AATGATATG AATGTTACAC
3251 ATCAATTCCC TGGTCTGAA ATACAGGTGAT AATGTCATC TGTGTTGTA
3301 CTGATTTAGA ATTGAGGGTA CAA TGTCTTGT GCTTCATTA ATAATGTTA
3351 ATAATTTTAA TTATTTTGA CTAITGGTCC TCTTATCTT CTAGATTC
3401 TCTTTGAAT TTGTTAATCC TCCCTGTTG TGTGTTGTTT TTTTCTCTC
3451 TAAAAGTATC CTCTGGGCAA GCTTACCTAC AACTACTATG GCTTACGCT
3501 CCAAATATAT GCCATATACG CAGCTTTA AGTTTCTCTA CCAAATTC
3551 GATAATTATA TCTGAATGTC TACGGCAAGT TCTACTGGA GATTAACGTT
3601 GCTCAAATTG CCTCATTTAT AAAAGTAAAC TGTAAATGTC TAACTGAA
3651 CTCTCTATCTT TCCCTGAAAC ACGCTCTCT GCTCTCTAA TGTGTTGCT
3701 AGTGAAGAAC ACTGTCTATCA TGTAGCAACT TACTCAAAG GCGCTGGTG
3751 TAAACTTGA CCACATAGC CAACTGGTCAG TCTATATCG TTGGTGTGAC
3801 CTTATTATG CTTCAATAC AACTCTTTT TGTACCCAT TGTACTGCG
3851 TCCTAAGTTA GGCTCACATT AAATGTTGAGA CAGGGAGAGA GCGCTGTT
3901 CTCTCCCTGT CTTAATTTT GCTTCTCT GCTCTGCTC TAACTGCT
3951 GCAAGAGCAA TCTCTTACAA TTGTTAATG AATCAATTTC CAACTTAA
4001 TAAAGCCCTT CTGCACTCTC GCAATAGCC AAGAGAGAAAG CAAATTAAC
4051 ACACGCTGG GCAAGTAAGG TGTGTTGTA TGTGTTGTTG AATGCGCT
4101 CCTGTCCTGT TTTTGGCCT CTCCTATTT TTTACTTGTG GCTTCTCTC
4151 ATTCCTGCTCC AACTGGCTGG AATGAGTCAC CTGCTCTCCG TGTGTTGCG
4201 TTGACACCTC TCATCTTCA AGAATCAGCT CAAACATGAGG TGTGTTGAC
4251 AGCCTTTCC AAATTAATCTC AUPCCCCAT GTAGAACTGA CTGCTCTCC
4301 TTCATGTACC CTCTCCCTGT GCAATGTTA ATTACGOCAC TAACTAGGT
4351 TAATGGCCTC TGTGGTCCCA CCACTGCCA CATTGTCCTGG TGTATAGTG
4401 GTGCACAATA GTTATTTGAT AATGCAATTG ATTTCCACA AAATGTTATA
4451 TCAAAATGTA CATGATTAA GATGCTCAGA AGGGAAATT TTGAACTAAC
4501 TAGGCGTGAATAGAATA TTGTTGCTCAA ACAAAAGACTT CTGTTTTAT
4551 TTAACACCC CAGGAAATC CAAAGGAGA AACAAACGTT GTCCTCTAA
4601 GTAGCTCAGT GCAATGACT TTAGGGATGT CGGACTAGAG AGGCACACTGA
4651 GATGTAATT ATAGCATTTT CTAATTAGG TGACCCCTGA AGAAACACTA
4701 GGGTGTAGA AGACAGGGCT TTGAGTCTG CAGAGTACTT GCTCACTTT
4751 AGAGAAAGCTG TTTGCTCTC TTGAGCTTCA ATGGAAAATG TAAAATGCGA
4801 AACCAACAGC TGCTTTCAA GGATGAGATG GGTGACCAGA ATATAGATGA
4851 CATTCAATAC TTTTTTATTA CTTCTCCTTC ACTGCATTAC CCTCACTAA
4901 TTGATTCAA CCTGAGGATG TTTCTGAAAG GCTGCACAC AAATATGAGC
4951 TCTGCCGAGG TTGACAGAGT TAAAGGGGAC ACCCTCTAA GAACTGTCAT
5001 AGTGTCAATC CACTTGATCC TCAAAAGCCA GAGTAGAAAG ACCATGAATG
5051 CTTTTCTTAA GCTTCATGCA ATGTGTTCCG AACCACTCAC AGTGAATTAC
5101 CTTTTATCTC CTGGCTTAA CATAGGACAT CATTGTCAG TTTTTAAAT
5151 CAGTTAAAG AGATGGGTT TATCTATGTG TGGTTTGGAT TGAACCCCTTA
5201 AATGTAATT TTTGAGAAAT TCAACATAAT GTATTTATTT GTGATCATTA
5251 TACTTGTGTT TTCAATACAT GCTGGGTTG GTATCAAAC ATTTAACATA
5301 CTGGGGACAT TTCTCATCTA TTTTATACAA TCTTGGCATG TTAAATGACT
5351 ACAACTCATC TCATGCCAA ATAAGAACAT GCAAATGCT CAAAGAAAGA
5401 AAATCTGTTT ACTTCAAAT TCTCAATTTC AAAAACTACT ATGGAAATACA
5451 GATTTAGTT TATTGATTAA AATAAAAGATT CCAGAGTTA AATGCTAGGT
5501 GGCACTTTG TTTTATAGT CCTCAGGCC ATTTTACGCT TCATTTATC
5551 CTGTCATCTC AGTCTCCAACT TGTGAACATT ATGTAACAGT CTGACATAG
5601 CAGGTACATT AATTACAGAC CATTAAATGTA AACCAACAAA GAGTGGTGGG
5651 CAGTGGGTGG GGGGTGAATG GAAATGGAAA GAGGCAACAA CAGGGCAT
5701 TGTGTTCTC GTGAGAAATA TGGGGAGAAG GCTAGGAAT GTTCTTAAC
5751 TGTGTAATCA GAGCTATTAA TCCCTTGAGT TCTAGAAAAG CACATACAC
5801 TTTGTGGTTT CGTGTGCTGT TTCTATCTAC ATCTCATACT GTTTCTATT
5851 CTCAAAAGT AACCTGTC TCTCTTTCC TCTCCAGATT ATTTTCAGGA
5901 TTAGCTCTG TTATAAAAAA TAGCTTGTAC AGATCTCTA CAATAATTAT
5951 TTCTATTTT ATTTCTAAGG TTATTTTATT TATTTATGTA GATAGACAGA
6001 GTTTCACCTC TGTGCCCAT GCTGGAGTGC AATGTTGCAA TCTGGCTCA
6051 CTGCAACCTC TGCTCCCAAG GTCAAGCGA TTCTCTGCT TCACGCTCT
6101 GAGTAGCTGG GATTACAGGC GCTGGCACC AACTCGGGCT AACCTTTGT
6151 ATTTCTAGTA GAGACGAAGT TTGACCATGT TGGCCAGGGT GGTGTTGAAAC
6201 TCTGACCTC AAGTTACCA CCAACCTCAG CCTCCCAAAG TGTGTTGGATT
6251 ACAGGCGTGA GCCATGTGC CTGGCTCTA GGATTATATT AATAGAACAA

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6301 TCTTCATTA TTTATCTT CTTATCTT CTTTCATGT AGGAAATGTC
6351 CTAATTTT CAAACCTCA ATTGAAAGC ACTTTAAAT TCTATACATAG
6401 TCGACATTT TATATAAAA CAACTAAAAA GCTGTGACCA TTTTGAGTA
6451 TAAAATGCA ATGCCAGCAG CAGGCTTAT TAATTGAGGC TCTTAAAT
6501 GTGGTGTC CTGGCTGGT AGGCTCAAAG GGGCTGGCTT GTAACTGAG
6551 GAGCTGACCA GCAAGCTCT ATAACCAAAT GTGACATCTT TTAGCTTGC
6601 TCCAAGAAA CCAAAACAC AAAGCTCTGT GGATAAGTGAC ATCTTAAAT
6651 TTPCTTCCC TCGAAACTCT TTPGCCAGTT CATTGAATTC CTTTAATAAT
6701 TTCTTAGTT TCATTCATTA TCTGTTAATA ATCCATCTAC ATCTTAAAG
6751 TAATTAAAC ATATAAGCAC ACACAGAAAC AACCAACACA AAACAAACCT
6801 ACCACTGAAT TACTTCCAG TAAGAGATGT ATGTTATAAT GATGTTACA
6851 AAAAAGAAA AAGAAAGAAA ATACAGCTA CAGGGGCTG CTCGAGATG
6901 CTTGATGCA GGGGAGAAT GGGGTCTCCC CCTGGGTATG GTGGTATG
6951 GGCGTCTGC TTCAACTCTC TGAGCCACAG TTGGCTTATG CTTATTTG
7001 AACATCAGAT GAGATAAGGA TCACAGTGC TAGGCATTTC ATAAATATTC
7051 GTGAAATTAA TAAATCATC TGATTATGGT ATGGTAACTG TTGAAATAAT
7101 TCTGTCTAA CCTCTACTC TTCTTTGGA AGGGCTTAA ATGGAAAC
7151 AATTAGTTGT AGTCTCTGC ATAGCTAATG TGAGAAAGG CTTATTTG
7201 ATAAACATT TTTAACTAA AAATAATAAT TCCTTCTTATP ATAAACATCT
7251 TCTTCATCC CAAAGTATAG TTGTAAATGG AACTCAAAT GTGTTGTTG
7301 GAATGACCGT TAGTGTGAAAG GAGGAAAGA AAATTGGGT CTCTTATTC
7351 CCTCCTCTG ATTCAGTTAC TTAGATCACC TGAAACATAC ATATGATTC
7401 GAGCATATAT TTAGATGTTT TCACTTTCTT ATTTGCTCT GTGTTGTTG
7451 AGTCAATTG CTAATGAAAG CACTGAAAGT CAGAAATTGC TCAAAATGG
7501 ATTTTGGGG AAAAAGAAGC TGGCAGATTA TGCTGATGAA CAACTAACTG
7551 AATCTATGCT TTCAGGCAAT AAACGGGACT GAGGGCTTCT CAACTAACTA
7601 GGTCTCTGTG GGAAACAAAT GTGACTGAAA TTTTCCAGG CTTGATAGC
7651 ACATTCTGTG TTTATTCAG CTCTTACTGG AATAAGGGCT TGTGTTTCC
7701 TCTTCCCAT ATCCTTCCAT CAATCAITTA TGAACTTAA GGGTTTGGG
7751 GGGAAATCAT TCTAACCCAA AGGTAATCTA CAATCATATA TGTTTCCCT
7801 TCTTATGTG ACTCCCTTG TAATTGTAT TTGACTGAG GCCTCTG
7851 AAACCAAGCA CTGCACTGG TTGAAAATTA CATGCTTTA TTGATGTGA
7901 GTAATGGCT TACTCTGTG ATGTTATCTT AGTCTTCAAT TTGCACTGT
7951 AATCTGCAGA TAATGTAGA ATAAGGATAA CCCCTAAAGG TATGCCCTT
8001 GGCAAATGTT TGCTTAAAT ACATCCCTTC TTTTCAAGC ATGGCGAAC
8051 CACTCCCTT GGAATGTCTT CATTAAACCT GAGTAATGCG ATCATGGCA
8101 GTGGGATCCTT GGGCTGTCC TATGCCATGG CCAACACAGG CAACTAACT
8151 TTATGTAAAG TGAATGTATA TGCTACATT TGGTGTGAA GTCCATGCAT
8201 ACCTGGTGGC TTTTCAATT AACATCTCA AGTTTGATCT TTGTAACGT
8251 GAAGACTCAG AGGAGGCTAA TCATGGCACT TGGTACCGCA ACGATCCCTA
8301 ACCCAACGGC AGAAAGTGTG TGTGCTCAAT CAACCAAAGT GCTGGAGCAG
8351 CCTCGCCAGA AGAATTGTGT TATTCACTAA ATACTGAAA TAATTTGGTG
8401 TTATGCAACC AAAAGATCT TTCCAGAAG CAAATCTGAT TTATCTCAT
8451 TCTTAGGAAA GAAGAACCA AGCCTAACAG CCCTGCATCT CCTGCTAC
8501 CTTATGCCC ATTCCTGTA CCCCTGTGCG ACAGATACAT TGCCACAAAT
8551 AGCCTCTCT CCATCTATG AAGATGCCAC ATCCCTCTP AGCATTGGAC
8601 CTTGACAT GGTCTGGAA CCCTCTCTC TTCCCTCTP ATCTAGTAA
8651 CTCCTCATAT GTCACTTCAG TCTCACCTGA ATACTGCGCG CCTGATCTC
8701 CATGACTGGG GCAAATCACC TTATCATAAC ACTCACCAAA ATTTTAATGT
8751 TTGACTGCA TTTGCTGAT TCATTTGGTT AATATCTGTC CCTCTTGTG
8801 GACTATAAGC TCTAGAAAGT TGAGCCATG TCTGTTTTA CTCACCAATG
8851 TCTCTACCTC CAAACCTAGA GCAGTGCCTG GTACAGGCAA TATTTGTGA
8901 GTGACCAAC CTTATCCTA AACCTACGTA CTTTCACCAA ACTTGTCAA
8951 ATGCTGCCTA AGGCTAGCAG CATCTGGTAG TTGACCTGTA GGCTGGATAC
9001 TGCACGTCT ATGACAGACA ACAACAGACG TTATGTGAA TCATGTACAG
9051 CCTGGCATTT TCCAGGATAT AGTTGGCAGC AGTGGATTG TTGACAAGAA
9101 TAAAGCTGTA TTGTTAGGCAC CACTGTGGAC ACAGATCTA ATGCCAAATG
9151 CAACGCTAGA GAGTAAATA ACTGTCTAAG AATGCAACAT TTATATCACA
9201 AATATGTGCT GTTTATGTC TGAATATCAC ATATGATTAG TAATCACACA
9251 GCTATTTGAG GGCTAAGCAT CAGGACTATA AATATTTGTA TTGTTGTTAGT
9301 GCTTGATTG AACTCTTTA TGATAATAT TCTTCAGCTG AATGGTTTT
9351 TATATCACT TTATTTTAT ATAAGCCATG TTTGAAATA AACTAGGATT
9401 TTAATAATCT GAATTAAAT AGTATGTAT GTAGTCATAT ATTTGTATGC

3451 TTTTGTAATG TGCTTACCTC TAAGACAAAAA AAACCTGCCT TTGTTTATTA
3501 ATTATACATA CCTTTAAATG CAATTAGGA GTTA TACATC ACTCTATGAT
3551 AGAAATAGGA AAAACTGCC CCAATCCAC AGTCATAGAT CATCTTCAG
3601 AGAGAAGAAAT GTTCCACTT TTAAAATGAG GGCCTCATT TAGGCTTATA
3651 AACACTTACG AAGATGAAAT GGTCAAGAAC ATTAAATGAG TAAATGAT
3701 GGGGTGTGTT TTGTTGTT AAGTAGGCCA GACTGAGTA AGCTTGTGTT
3751 CTTAAATTATG ACGATGTTTT AAAGGTTTTA CCTTTAGAT
3801 TTTCCTGCGAG ACAAATATA TGTCTAGAAT ACAAGGGAAAGG CTATTATG
3851 TTCCAGGAA CAAAATATA TAATCTGAAT TACATTATGCT CTAAAAAGCA
3901 GTTAAGTTCA TAAGGCTAT GGAAAAATAT AGGAATATGCT CATGGTTAG
3951 ACAGTTCTGG CAAAWATATG CTATGGAAA TAAGACAGCA ACATAGCTAC
40001 AGGGGTATAA AAATTTATAA TTCTATGGTC AAATGTAATG TTGTTAGTATT
40051 GATTTTCATTG GAAATTACCA AGGGATTAGA TCAATTGTTG CGAAAGTGTAA
40101 TTTTTTAAAG ATAAACAAAG ATAAAGATTT TTTTCTGCGAG TTGTAAGTAA
40151 AAGGCAGCAT TGCTTCTGTA TTTATTACGT AGATGCTTCT ATCAACATTC
40201 TTATTTTTGT GTCGAAATG TTGGATTGAG AAAATAAGA ATCTGATATA
40251 ACATAAAAGAA AATCATATG CATGTGGGAA TCCAAACACG AGAAATGAGT
40301 CTGAATGAA AAAAAGAAAAA AAAAAAAAGGGAAATTTTCTGCGAGGAG
40351 CTTAGCTTTC TTTGTTTCTT CTATTATATA TGCACACTGCTGCGAGGAG
40401 CCTTACAAAG TACCTTGTAA TCTAATGCAC AGGATCAAGCA GCAATGCGAGC
40451 TCAGACTGCA TGCTTCTGTC CTTGGATTCC TAGATTTTCTG ATTAAGGTTT
40501 AGTCAGGTTA TTGAATAGGC CTTCAATTCT AAGTGTGATG GTGAATATCA
40551 TGCAAAATG ATGTAATATG TCCCATGTG TGAGTAAAGCA GATGAGCAT
40601 TTGCTAATGT TGCTATACAT TTAGCATCTA AGTTATGAGC CAGATTCTAC
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40701 GCACAAATCTA TTCTATGAG TTTAAAGGGT ATGTTGTAAGS TTGCGAAAAG
40751 AATTCTGAG CCTCCCGAA ATCCACACATG TTTGCGAAAAGGCGAGGATTG
40801 AAAAGATTA TGTGATGTT TATTGTAACA TCTAACATAA TTACATTTTA
40851 TTTATTGTTG AAACTTTTAC ACCIACTCTC TCTTCGTTTCTGCGAGGAG
40901 GCTGCTTGCT GGGCAATAT TATCACTGTA TCTCAGTTGAC CTTTCATTTAA
40951 AAACAGCCAA GAAAGGAGGT ATGCTACAC TTGAGTCAAGA CACATTCTAT
41001 TTTAATTCTC ATAAAAGAGT ATTCAGTCT GTTGCTTCAT AACCTTAGGA
41051 TGATTATAGT CAGTTTCACA TTTCATTTTC TTCTGAGGCC AGTGACACCGA
41101 TCTCTCAGTG TTTATAGTTG TTGGGGCAAG TGAGAGGCCAG GAGTGAAAGT
41151 CAACTGGCTC AGGTTCAAGA CAAATAGAAA AAAGAAATTT CTGATATATG
41201 ATAGAAATAA CTGTTTGAC TTGCTACATG CAGCTAAAT AAATAAAACG
41251 ATTGATTCTT GTTTGGAGAA CATTGGATA TATTGCTTAT TGGTTTTGAG
41301 GGTTGCATCT TTTGGGCTTA TAATTCTAT ATGATGTTA TTTACATGTT
41351 TGAGACTCCA GCAAGAATT ATATGACAAA AATATTTAG TCATTAAAAC
41401 AATCTCTTA AAGGCTAT TTTATCTTG ATTGTAGGGT CTTTGATTTA
41451 TGAAAAATTA GGAGAAAAGG CATTGGATG GCGGGGAAAAA ATTGGAGCTT
41501 TTGTTTCCAT TACAATGCG AACATTGGAG GTAAGGGGAT ATACTTTCCA
41551 ATGGATCCCA TAAACCTTCT ATAGCGTGTG CAATAAAATAA GAAAACCTTAT
41601 GGCAATAAAC AGGCAATTGATGACAGAAA ATTGCTAATG TATACTTCTT
41651 AAATTTTAAATGATGATGTTT CTTAAATAGG TTGTTGCTTCT GCTTTAATTA
41701 AAAACAGCAA TATCTAAGAA TGAAATAACA TATAAAACCG TGCCTATTGAA
41751 ATTCTAGAAAT TAAATATAA AATAAAAGCT TTCTTGATTTT TTAATGTTAT
41801 TATAGCATGA ATTATTAATG TAAAAATG AGAATTTG GCTTATATCT
41851 GTCATTGACA AACAGTTGA CGTTTCTAT GTGTGACTG GTCGATTTA
41901 CTAAACTGAA AAGGGGGTGT CTGGGGGAAC ATAGCCAAAT GCTGTGGTCC
41951 TTGAAACGCA GCTGCACTG AGCCAGCCCA CTAGACAGTG TCTCTGGAAG
42001 TTTACTAAGG CAAAAGCTG GCTAGGCATC AAATGCACTA TAAACCCCG
42051 TTTGTTGATT CTATGGATTC TTATAATTCC CACTGAATTA TCAATTCCAG
42101 TGTAGGACCT AGAAATATAT ATATATATTT TTAACAAATGT TCTCTGTTG
42151 CTGTGTTGCT GCAACAGCTT CATACTGTTT CTGTTGTTGCT TTTGGCCCTC
42201 AGAAGGCATC CAAACCCATA TTTCAGATGT CCTGCGGGGT GCTTCTGGC
42251 ACATGGCCCG AGCCAGCTGC CCACATAATG ACACCTACTC CTTCACCTCC
42301 TACCCAGTGC TAAACCTGC TATCTTATTT CTCTGATCTT TCTTTCTCA
42351 CTGAATACCA TAAAGCAGTCA TCCAGTTCT GAGGGCAGAA ATCTGGATGT
42401 CAGCGTAAAT GTTTCTTTT CCACCAACTCT GCTATGTCAA TCAAATGGCA
42451 AAGTCTGTC ATTTGATCTC TTACTTATCT CTTGAAACCTC TCTCTGTTG
42501 CGTCCTCAT GACCACAGAT GATCACCATT TATAGCTCAG ATTATTGCGAG
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1.2601 ACTCTAATTT GTTCTCCAGA TAAACTTTCT CAAATTGAG TCTGTTCTA
1.2651 CTTTGTGCGT GCATAAAATT CTTCAGGAGC CTTTATTAT TTTCAAGGA
1.2701 AAACCTAACAC TCATTTGAGT GACATAAAGA CTTCGCTAG TTTCTCTGCT
1.2751 CAATCTTCT AAACCTTGT AGCAATGCG ATATCTATCT ATCTTTATCT
1.2801 ATCTATCTAT CTATCTAT T ATCTATCTAT CTATCTATCT ATCTATCTATC
1.2851 AATTTATCCA TCATCTATAC CCTACATGTC CTGTGTCAAA CCATAAATAA
1.2901 TTATATTCTT TCCCTCTAA GTACTATTTT AATATTCTT AAAATCATCC
1.2951 ATGCTCTCTT TTTCACAGGT ACTTCTCGCC CTGACTGTC TCTCAAGTC
1.3001 CTCCAACTCT AACACACATG CAACACACACACACACACACACACACACAC
1.3051 CACACACATT TTCTCTCTA CTCTCTCAC CTGGCTATCT GCTCTCTAG
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1.3151 TATGTTACTG TTTCTAAAG GATAATTAA AACACCTGAG TAGAGAATAA
1.3201 GCTTTGGAG TCTGATGGAC CTGAATTGAG CTGCTGTTCT GTCACATCTT
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1.3351 CACATAATAA GTGTTCTGTA TATGTTCTC TCCCTCTGG TTCTCTGCTT
1.3401 CCATATCCAT GTCTCTGGAG TTGCTCTAAT TATTTTTAA ATAAGCATT
1.3451 AAAAATTAT AAAACAAATA TATGATGATT GTGAAAAACT AAAACACTGC
1.3501 ATAAATATAT AAATTACAA GAAAAGTTA TGTCAGTCAT CCTAGAAGAAT
1.3551 AACTACTCAT AGGTTTCCC CTATGCTAA TTCAACAAAT ACATTGAATA
1.3601 TTGTTAGTAT TGGATCATCT TATGATACCG ATTTTCAGCT TTGTTTTAA
1.3651 ATTTAACAAAT ATGCCCTGAA TATATTGCA TGTTATTCTT TTTATGATT
1.3701 TTGAGGTTT CCATTACACA AAATGTCAT AATTTGTTA CAGTATCCTT
1.3751 ATTGATGAAC ATTTGGATTG TTTCTAATTT TTCACTGTTA TAAAAATGCT
1.3801 ACAGTAATAA CACTTGACAA GACATTTGC AAACAGGCAA CCCATTAA
1.3851 TAAATAAATT CACTGGAGTT ATCAAGGATT TCTGGAATGC AGAAATTCT
1.3901 TTACTAATCT ATCTAATCT ACTCACCCCTG ATAATGGATA GTGCTAAGC
1.3951 AGATAAGTAA AATTCACTA TATCTTATGA TTGTTGTTAA AAAAATT
1.4001 ATATGTTAAG ACTACAATCT TGGTACAAAT TGCACAGTAA TATCAAAATT
1.4051 GTCTCATCTA TTTTACTGGT TTGGAGGCCAT ATGCATATTAA GCCCCC
1.4101 TCCAACAAA TAGACCACTT TACATTGTT TCAAACCTCTC AGCUTTATCA
1.4151 AGGTTAAAG TATCGAGCAT TTGATAGGAT TGCTTATAG TTGCTCTAAT
1.4201 TTAACAACTG AAATAACCG GCATAAGCAT AATTAACCCCT GGACTCAAGA
1.4251 AGTTGAGTGG CAGCACCTCA GCTGTGGTTC AAAGCATAGC CACTACTACG
1.4301 CTTCTAAACA ATGGAATAAA CTATAAAGCG GTCTCTCAGT CAAGCCTCAC
1.4351 ACAGGTAAGA GGCCTGACTT TAAGGGAGTA AGATGAAATA TCGTAACATC
1.4401 ACCCCAGAAA TAATGCTCTC ACTTTGGTTA CTTTATTGAA TTGTTGATA
1.4451 TTGGCATAA GAGAAATCAC TTGTATTCT CTATTTAAC ACTCTACATT
1.4501 TAGAACACTT AATTCTCA ATCCCCTAAA AAATTAACAT TTACTGCAGA
1.4551 TGTTTCACA TTAACAGATT AATGTCCTGAA TCATTCTGAA TTTTGAGA
1.4601 CAAACATGT TAACATCACT GACATCACTG AAAACCAGCA ATTAATAGCT
1.4651 GTAACATTGA ATGGTACCTC ACCAAGGCCAG CTAATCAGAA ATATCTCTG
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1.5351 TCTTCACAA GAGTAGATAA TCATTCATGT ATCACTTACCA TAGATGCTCA
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1.5451 GATGAAGAGG GGGGAAAAAA AAAACTTCTT TGACAAAGAT GGAGAGAAGC
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15751 TATGTTGATT TATAACTAAT GAGGCCAGAA CCTTAGAACT GCAGCTTCA
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15851 CAAAGGTCCA CCTGAAAGAG CTGGAAAGTC AAATGTCTAT CTTGGAAAGAG
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16051 TGTCAA-GCTA CCTCTTTATG ATAAATATG AACTACCTGA AGTAATCAGA
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16251 TTGTGTCGTG TGGATTATT CTTOCACTTT CGCTCCTTAA AAATTTA-GT
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16751 TTTAGAACAG CAGAGGAGAG TCCAGATGAA GAAACAAGAA GGCTATATC
16801 ATATTCACT GAATCAGCCA TTCTCTTAA CACATCCAC CCATTAACAG
16851 AGGACAAGAA CAGTGGGATT AAAGAAGAAA TCCTCCTCTC TAGGCGCTG
16901 ACAAAAGAGG GAATTCTTG CACTATCATG AATGCCAAA TTTATAAAGC
16951 ATTTCCCAA ACAGGTAAG CAGAAGGAAA AAAAGTTTG AAGACCCATG
17001 TCACCTTAGT TTGAAGAAAT AAGGAATGAA TCATCTTCT CATGGAGGG
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17101 AAGAGGCAAG GCTGCCAATC ACAGCTCCAA CTCTCCCTT AGAACAGAGG
17151 CTACAGCCAC TTTCTTTCT CCATTACTCT ZAAAGGAATC CTTAACTGAG
17201 TTCCCTCACC CCCCACCTA TAAGCCACAC ATATGGATTG TTATTTCTT
17251 GTTTTTCTC AAAAGCTGA TTTTTTTTC TTTTTAAATG ACTGAGCTA
17301 GGTGATTAC AAGAAATTCC AAATACCTG CCCTCTACCT GTTTGGATC
17351 ACAGTGTGG AAATCTGTCA TTCAACAAACA CGCTTCCAAT GCATGTGTTA
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17451 CACCCACCGC AATCTGCAG GGCTGGATGAA GAACCCAGGCC AAGGGCTCTC
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17601 AATGAGTACA GTTATGTGTT TTCTAAGTTT TTATTCAATA AACTGAGATG
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17851 ATTCTTAAC AGGAACACA GTTATAGCT TCCTCTTCAG AGAAAATATG
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17951 GCCCCACACA GCACTACCTT ATCTCTTTTC TCTCCTTTCT CTCCACCATA
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18051 AATAATTG GCAGGTGTTG GGAATTAAA TTGAAATTGTT GTTCGGAAAGA
18101 AATGATGTCA GCTGGACTAG AAATGAAAAC ACCCATGACCC ACCAAAATTT
18151 ATGGTTAGGG GCAGCCTCGA TAAGCCAGTG ATGTCATTAA TAGTCAGCAC
18201 CTAACCCCTG TCTAGAACAC ATTCAATTACA AGAGATGTGT CAATATCTGT
18251 CCTTTGTGTT CTTATTGTA CAATAGAGTC ACTGGCTAGA AAATCTTGT
18301 TCTTCCAGCT GATGGTCTAT GGTCTATTG TATTCTTTTC CCTTTGAAGT
18351 TGTTGATATT TGCTGGGAA CAAAGGATAT GAACTCATTAA TAGCTGTTT
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18601 GAAGCCTGAC AATTGATCTT TGGCAGGCCAG GTTCTCTCA GAATGGTTTT
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18701 CTACTAGTTT CTTTCCCTCA TTTAAAGTCA TCTCATTATG AAATGAAAAA
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19151 TCTTGGTTA CCTAAGCTT TATGAGGT CACTCTGAAA GTCATIETJT
19201 ATATGCAAAT CCTTGTGAACTTGGTCTTG ACCTGGGTAG GATGATTTTT
19251 TAAAAATTCG CTTCTATAAGTATGTTAT AGATGACACA TATTCAATTAA
19301 ATATACTATT TTAGTTTGT CACTTGAGCT GAGGAAATGG GGCCTGATTC
19351 AGCCTGGCTA CAAAGTTA AAGAATTGCTG AATTAACACG TATTTTATAA
19401 AAAATATCCC TCAAACAAAA TATTTTCTG CTAGGGATAG ATGATATTTC
19451 TCTGGCTAGA CTCCATACTG CAACTCAGGC TACAAGTGT GAGAATGAAAT
19501 CCACTTGCTAT GTGATAAAGT CTTTTGATG GAATTATTAA CTGOCAGAA
19551 AATAGCAGGG AAAACTGGGAG GGCCTCAAGT TTGAATTTCG CTGCTCTTA
19601 CCAGTCAAGT CAAATCTGG AGCTGGGAC TTTAGGTAAA ATTTCGAA
19651 TATCCCATTG TATTTTGTCA TACTAAATGAA TTTCCTAAGA AAGAGGACAT
19701 GACAGAATTG CCTTCATATG TAAAGATGCAAC CACCAAAAAA AAGTGAATT
19751 GGCCACATTA GATTATGCTT GAAACATTTC CTCTCTGGCA TCTTAACAGT
19801 TCAAAAGGG AGTAGGATTC TACTCTTG ATGAAGTGTG GCCACATAAA
19851 CAGATTTCAT GGAATCACAT ATTGACCTGG TAGCATATGT TTACATGAA
19901 CAGTGTATCA ATATAAAATAT ATTTTTGTAT AAACCTCCTT TTAAAGTTT
19951 TAACTTAATT TTTTCTTAC TGTGTTGGTA AATTGAATTG CATGTATGAC
20001 AAATTGTGA GGAAAGAAT CAGGAGTAGG CCACCATTTG CTTAGGTTT
20051 TTTCTATTT GACTAATATT TRACTATTAA CCAAACATGT GCTTTAGATT
20101 GGGCATTAAC TTTTGCCTG TGTGAAATA ATGAATGACG AGGTCAATAC
20151 TACTGAAGGT ATTTTCACTA CTTTTTGTCT GATCTTGAGG TGAAAATCCA
20201 ACTACGCTTG ATTCCATAGA TATTTTCTTG TTATTGTGC TTGGACTCT
20251 GAATGAAGGT GTTTCTAAGT AGGGCTGCAT CTTCGTCTTA GAGTAGTAC
20301 CACTGGGAGA CCTCTTAAATTTATTTTCTG CACCTTACTT
20351 ATACTTATT TAATGACTT CATAAGACAA GCACAAACTT GAAAGAGCCC
20401 AAAATATCT GTTTTCTGTT GGTGATGGAG TCATAGTTGT TGACCTTGAA
20451 AAAATGTAG CAATCATTCA TCTAGAGTT TACACACTGG GTTTGTAACC
20501 TGCATCAGGA GTGGCTCCAG AGTAGGGAC AGGGGAGGTG GTAGGCTGGG
20551 AGAGACAATA TGTGGGGCTT GGGCTCTCA TCCCCCTCAA CAAGAGCACC
20601 TTGGTCTCTG TCTGATTCT AATTGCTTCT GTACAGCGGA GATAGATTAA
20651 TCACAATGTA AATGAGCTTG AGAGGCTCTT TATTTTGTAT TATACCTTCT
20701 GCAACGTTAT CAGCTCAGG ACCTCTTTGT TCATTTGAAT GAAGGTTGCA
20751 TAGCTAATGTA GCTCAGAGGC AGACCAAGAG GTGCCCTGGAT TCCCAGGCCT
20801 AGGTCTTTC CTCTGTCTG TGTCTCTCT ATAAAATGTT GCCATAAGTG
20851 ACCTGTGCTG ATTTGACAAAC ACCAAGCGGT TTCATTCTCT TTTTCTGTT
20901 GTAGGAGAAG TTGAAGATGA ATTACTTCAT GCCTACAGCA AAGTGTATAC
20951 ATTAGACATC CCTCTTCTCA TGTTTGCCTG GGCAGTCCTT GTGGCAGTAA
21001 CACTAACTGT GCCCATTGTC CTCTTCCCAG TAAGTACATA AGACTTTGAT
21051 GAAAGAACCC TACTTGACCC CATAAATTAG TACATGTGTT CTACCTTCAT
21101 TTTGATTAA TTATAGGGTG AGTTTGCAT TGCAATGCC GAGGATATTA
21151 TTTTCTTAA GCATTTTGAG TCACTAAAA TTGGCCATT ATTGTGTAGA
21201 TAGAGCAAGT AGTTTCAGGT GTTATTTTA TAGTGTAGGA AAAAAATCAT
21251 AAAACTTATT TTAAACTCA AAGTTGAAAA GTGGAGCTGG AGCTTCTGTC
21301 TTGTTGATTA GTAAAACGTA GTAGGAGTTC ATATAACTTT GGAACCTTGA
21351 AAGCCAAAC CATATAAAGT TTCAAATCTT ATAAATTTT ATCACAGTTT
21401 TGAAGGCATT TCATTTTTT TGTGTTGT TGTGCTGCAA TAATATACAA
21451 AAGTTGCCTT TTTAACCTG ATGCCCTGAA GGCTAATGAA AAGGGGATTC
21501 ATGTTAAGTA AATTATATAC CAGAAAAAAA TTTTCAAAA AACAGTTATG
21551 CTATCTATCA CATATCTCTC TCACACATGG CCTCTGCCAG ACTCACACCA
21601 GGTCACTCCCT CCTCTGGCAATT TGTCTATTGGT GTCAGTTGT TCTGAGATCC
21651 CAGAGCAGAG CTGGTAGTGA AGATTTGGGC TGTGTGAGTT AAAACCA
21701 CCTAAGGATA AACACAGGTC TTCAACCTCC TGCCAGCTCC TGTTCTATAA
21751 AACTGAATT TACTCATTC TTTGAGGGGG AAAAAAATAA GTGACACAGT
21801 AACCAAGCACT GTCCCTGGACA TAATGTTCCA TACAGGGCTG GCATATGAAG
21851 ACTATTCTA TAATGACACT GTGGTCAATT TAAATGCAGC TTGTGTGCTG
21901 AAATATATTT TGGCACATTG CTTTTCTATG AGTGCATGAA ATCAGATCCG
21951 TACTACTATG GTGGCTAATA TTTTACTCTT AAATCATGTC TTGCTCTAA
22001 TATATCTGAA AGTATTTCAG ATGACATACA CATAGCTTTA GCCTAAAATC

23051 AGCTCCGTCT TGGGTACAAG ACAGAAGACA ACTATAAACCA GAAGGTATAAC
23101 GATAGGGTAA AATGCCAGG CAAACAACCTT CACTGAGAAA AGGATATCTG
23151 GAGCCCTCT TTTATGTGT AAAAATCA CTCCTAAAT TTTGGCACAG
23201 TGTAAGCATT CACATCAATG TAGAATCAA GCTAAAGAAA TCGTGATGT
23251 GCTTCTGTAT TGTTTATTG ATATTCATAT AGTGTGTTCA AGGCTAGGTT
23301 TTAAGGATT GGAGAATG GCAATGTCACAGACAGC TGCTAACAGT
23351 TCAACTAGTG CAGCTCATAG CCAACACTG AGGGCTGCAA TTAATGTCAT
23401 GGGAAAGTAA AGTCATTAAC TGATGAACAT TTCACCTCAG CAGGGAAAT
23451 CCAAACTCTCC CCTTAAAT TCTTACCTA TGTGAGAAAT AAAGCACTGA
23501 TATAATCTG AGCATCAGA ACAGCAATAG TGTGAAACCA ITAGATGCGA
23551 TTAGAACCAA AATTGACAT AAAAACCGAG GTTCAGAAAA ATGACTAACT
23601 GCTGTCCTTC ATTATGTTT TCCACTAAC ATTAGCATTT ATGAAACATT
23651 TTGCACATTA TTTGTCCTA ACGCTTCAA TTGTTACATT ATATAATCTG
23701 TGTAAGTGCT CCACTGCGC ATAGAGTCAT AAGTCCCTGG GACTTGGTGA
23751 TGTGACAGT GACTGGACA GAGGGTGAGC TCTGTCGTGC TTGGAAAGAA
23801 AAATGGCTT CAAATGAATC TTGCTTGTGTTGAAATGTA TAAACTGCCT
23851 TTTCTAGCAA AAGCATAAGC ACGCTTCCCG TTGGTGACAT GTGCTACGAA
23901 TTCAGCTGGG TTGAGGATCT GGGCTAAATG AACCAAACCT CCCTATACAT
23951 GAAGGATACA CAGACATGTT CAGAGAGT GGTCACTTCC GTGAGTGCAT
24001 CTCAATCAAG TCTCTGAGG CTAATTCAA TTTTTTTCT TTACTAAAT
24051 GATAAAAGTT GTTATTGCGG CTTTGTGTTG TTATTTCTG ATAACTTACGG
24101 GCTCAGATTT TCAATGCGC AAATGCTGAC TCACAGCATG GTTCTCTG
24151 CAGTTTATTT CATTAAAGG ACTCTTCACC AGTAAGTTA TTTACTTGC
24201 TTGATATCTC CACACATTAA TAATAAAACT AACAAAACCT AATCTGAATT
24251 AAAATCTATC AGCTTAGGSC ATTATTTGTGTTCTCCTTC TTTCAACATG
24301 GTAAGTGGG TCTCTTTTGT AGGAGCTGGA GAAGATATGAACTGGGTTG
24351 TTTTCTCTA CTCATTTAT TATCTTTCTT TTTCCAATC AGGTTAGTT
24401 TTTCTTTTGT AGTAAAGCT GCAAGTAAAC TGCTTGAGT ATTTGTTGAA
24451 CAAGTGAATA AATGAAATCA ATTAACCTAC TCTTTTCAGT ACCNCCCCAA
24501 CATTCTTTCAG AGGACTGATC ATGTCATTTT CACCTTATGC TTCCCTTAT
24551 CTCCCTCCAG AGGACTGATC ATGTCATTTT CACCTTATGC TTCCCTTAT
24601 GCAGTAAAGT TTCCATAATT CCATAAAAGAA CAAGAAACCA AATAATCTA
24651 ATGGATATAT AATGAAACACA CAGATGAAA TTTCACCTGC CATGCTTTG
24701 AAAAAAGATC CCTAGCTACT TGTTATTCAT CTTATAATTA AAATCAGTCT
24751 TTTCACCTAT GTTTCTCTA GATCTCTGT TTTGAAGTGT ATATAGATAT
24801 CAACATAGAA ATGCAGCGTA TATTGCTATC AACTGCAGTG GAGCAGTGAT
24851 TCGTAGGTTT TCCAACATCC TTGCTTAAAG CAAACCTGCA AAACTAAAGT
24901 GTGAGCTACG TCTAAACAAAT GGGAGAGGCT TTTTTTTTT TTTTAAGAGT
24951 TAGAACTAAG ACTCTCACTT CCTCCTGTGC CTCCACATT TTGACCTCA
25001 CATTGGGCCCT CGTCATCAGA ATACAGCACC CCCTAACAGG CTCTGTCA
25051 GGACTCTTTC TCTGAAATA ACAGATGTTG TCTCTAGAGC TGCATAGAAC
25101 CTTAATGAA TCATGTTGG TCAGAGGCC TGGATGGTGC TGGGACCTC
25151 CCTGACCCAC AGCATCTGAC CCACATTCC AGGTTCTAG CGACTTGTGT
25201 CAGTAAAGAA AAAGCAGAT AGCTAAGTGG AAGAGCAGAT GAGGCTTGGT
25251 GGGAAATCAGC CAGTGGCTG CCTAGCAAA GGTAACAGA ACTGCTGGGG
25301 GCTTTGGTC CTAGCTCAC TACTCAGGGG GGCACCTTAA CATGGAATGA
25351 CCAGCAAGT TTCTCTCTA TCTTTTCCAC CACCACACA AGCCTAGTAC
25401 CTCCCTCTCTT TTGCTCTCTT CGGGATGCA CTGGAAACCA
25451 CCTCAGTTC TGTGAAATTTTCTT CTTACTCAGA AAGAGGAAGA
25501 AGCTTTGCA TTTACTCAA CGGTTCTACC TATTATTCCTTCC ATAAACTTTC
25551 TGTGATCTCA TATCATTAGG CCAAAATGTTA ATCTTCTGG GAGCAGGAG
25601 ACTGCTTCA CATTAGGAGG CCTGGACAT ATAGGACTGC CTCTAACTCA
25651 CTCTAACTCA GCTTATTGAC TTGAATGCAC CTTTTAACAA AGTACTAA
25701 AAACAAACTG TGACTATTCT CTGAAATGA GCCTATATCT CATACTTATT
25751 TATTCTGTTT AACACTGTGA AACAAATTAA GCCTCTGGC ACTATGTATA
25801 TACCAAAAA AGCTTATTG TAAGCTACT AATTGGACCA GTTTGACAA
25851 TATTGAATAA GCACTAATTG CAGATCATAA TGAGAATTA TAGGCTGCTG
25901 AGGAAACAA TATCACACCA TTGCTTCC TCAGTTTCCCTTTCAGAATG
25951 AGTTTCTAA TGTTCAAA TCCAAATTAA AAAATCCTT ACAAAGTTAT
26001 TCTTAAACTA TTTCCAGAGA CTATCTGGTT TGTCTTCTA GAAATGAAAT
26051 TGCTTCTCA GCTAAACAG ATGGCTTAA TTTTGTTGG AGTGGTATGA
26101 AAGGAATGTC ACATGAGAAA CTGCAAGCTA TTTAGCTTGA ATTTTTGTC
26151 ATTCATACAT GTTCAAAAT ATATTTACA TTTCTCTCTT TTTAAATGAG

25201 TTCCCATCTC TGCACCTTAA CTGACTTCAG AACTAAAATT TTAAAGTGA
25251 CATCAATCAC AGCAATTCCA AAAATGTGAA CTCTTAGCTT AAACGAAAGTA
25301 TTCACTTATT GGAAAGCTGA TAGAGTAATT CCACTAAGTC CAAAAAGCT
25351 CCTCTAAAGG ATTCAAAAGA TAAGAGTGTG TTCAACTTTC CAAAGCTGTA
25401 CAAACACAAA TGTCACTGCC TCCCTCTGCC CACAGGGATC TCTATCCAGT
25451 TACAGCAGCC TAACTTGAGC AGTTGCTGCA AACTGAGGCT CTCTTGACCC
25501 TTGCGCTACT TATTCACTG CTGAAAATAG GGCGGAAATC TTTCAAGGAT
25551 CCTGAAGGGAG AGGATAAGAT CCTCTATTG CAACTTAAATT TAAGCTTTA
25601 TTCACTGCCT GCTGPGGCA CAACTAAGC CTGAAAGTC TGGGAATGTT
25651 TTAGATTATT AGGTCTGTT CCTTGCCCTT CATAGATTTA CAACTTATG
25701 ATAGGGAGAG CTAAAAAAGGA GAGAAAGAGG AAGGAGCAGA CATAAAAAG
25751 TCAAAATTTT AAAATACCAT TTAAAATTT TATTTTAAAGA TTTTAAATAC
25801 CATGAAAAAT TAAGGAAAAC CAAAGATTCA TAAAATTCCT TGCACAACT
25851 TGTGAAATC AATTCAAGGCG TTGECCTTAA TGTCTCATTC ATCTGATG
25901 GACATGTTT GTGATEAAAC AGGGTTTAC TATGTTTCTT AATTATGTT
25951 CTTGCCTGTT ATCTTCTTCTT GACCGAGATT ATTTTTAAAGA ATAAAATCTG
26001 AAAACTAAGA AAGTGAAGC ATAAAATATT GTCTTATAAA ATACGCCAAG
26051 GAAAAAATGA CACTCCATT CAAATATCAA AAGTTAGCAT CAAAGCTGCA
26101 CAAGATGAAT STACACTCAT GTGTTGCCCA CAAATGTGCA CAAATCTG
26151 GAAATGCATC TTTAGGCAAT TTGTCATTG TGCAAAACATC ATAGATTGTA
26201 CTTGCAGCCT AATTGGTGGCA CCTACTATA CACTAAGGCT ATATGCCATA
26251 GCCTAGTACT CCTAGGCTAC AAACCTGTAC ACCATGTTAC TGTACTGAAT
26301 AGTGGAGCTA CCTGAAACAT AATGGTAAGT ATTTGTTCTT CAAACGTTAG
26351 AAAAGCTACT GTAAAAATAC ACTATTACAA CCTTAGGGTA TGTACTGCTT
26401 ATATGTTGTC TGGTGTGAC CGAAATGACT ATGCTTAATA TGTACTGAATC
26451 GTACACTAA AAATGGTTAA GATGGTAAAT TCTATGTTAT GTATGTTTA
26501 TAATAATAAA AAAATGAAAG AAAGCATCAA CAACTTTCTT CCGAAAAAAAG
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26701 ATACGACATT TCTGATTGC AGCTGTCCTT ATTGCACTTA ATAATGTTCT
26751 GGTCACTCCTT GTGCCAACTA TAAAATACAT CTCGGATTG ATAGGTGAGT
26801 TTCAGAAAGG CTTCAATTG GTCAACCCAA ACTCACGCC CATTAAATGA
26851 TGGACAGGGGA ACCAGTGCTG GGTCACTCCAG ATCCCCGTTG TTTCTCAGGC
26901 TCATGGATTCC CTTTATCCC TGGGAGGCTC TGGTGTATCA GCTGCTCACT
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27001 AAGCTGCTTT TTCTGATAGA TGAGGAAACT GACCCCTATA AAAGTCAGT
27051 CATATACCTT GGTGTGGACC CAGGATTGG ACTTAGGTAT TAGCTCCACC
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27151 ACGAGTATCA GCTGAACATT GAAAGGTATC TTCAGAGGAA TAGGAGGTTG
27201 ATTATATAAA GTGTATTATT AGTATTCCC CATAACTGCA TGGTCTATTA
27251 ATTTTCATTC TACTCATTGA GGGTTTACTT AAACTTTAAAC CACAATCTAA
27301 AACTTTAAA GAACCATGGG TAGGTCACTT GCAAAGTAAG AGTGGATAG
27351 GGTGTGTCAT GAGTTCAAGC ACCTTAGTAT GTATTTATAT TACTAATCCC
27401 CTGTAATTT GTGTTAAATT CAGCCTTTTG TTGCTTATTA TATGTTGCAT
27451 ATACTTATGC AGCTTGTATG TTAGGTACAT TTTAATTGTC TCTATAAAC
27501 TATCTCTAT GAATAAATAA CCAAGATGAG CTTATGTCAG TTAAGTGTGT
27551 GTTTTAGTG CTAAGTATAG CATACTTTA TATTTGGTTT ATTTAAAGTG
27601 TGTGCTGGCA TCTCCTTGC TAGGAACTGC TGGGTAAGAC ATTGACCTTG
27651 CCCTGTGTTT GTCTTCTCAG GGGCTTCTTC TGCCACTATG CTGATTTTA
27701 TTCTTCCAGC AGTTTTTAT CTTAAACTTG TCAAGAAAAG AACTTTAGG
27751 TCACCCAAA AGGTGGGGT AAGTAAACCT TGCAATTTC CCCATTATTA
27801 GTTGTCTTC CAACTACTTA GAATAAACTA GAAAATACAC ATAGTTCAGA
27851 AAAATGAATC AATGTACAAG AACCAAAAT CAAAATGGG CTAGAACTTT
27901 CTGGTAGCAG AGAAAGGGGA CATATTCTG AAACCTAAAT GATTCTACTT
27951 CAAATATCAA ATATCTGTG TTGAGTCTGT CATACTGTC AAATAGTAGT
28001 AGCCTTCCC ACAGACACAT ATGCTTCAGG CAAATAGCG TGTCCAATAC
28051 CAAGCTGCTG TTGTGCTATC CGTGGAAAT CATGCAAGAA GGAATTAGGC
28101 TCCCTAGCGG TTGTTATGGAA TAATTTAAAT ATTTTGGTAA TGTTGTTAG
28151 GTTGCAAG CAAAGGGAA GATGTTGCTT TTGTTTCCCTTCCATAGTA
28201 CCTGTTGTCC CTGGTGTGGA CTAAGATCCA GAACAGAAAC ATTCACTGTT
28251 CTGTTAACCT CTTTAGATAC AAAATACAGT CTTATTAAAT TAGAGAGTAC
28301 ATATTCTTT TCCATAAGAC TACTATAGAA ACAATGCTA GAAATAATTG

28351 TTTTCCAAT AAGGAAATAT TATCTTCAC TCTTAATAA AGTCATGTTA
28401 AGGCTTGAAA AGAATATTTC TTACTGAATT ATTCGAAATT TTTACCTGCA
28451 AGTCATTTAC CTTGGGATG TTCGGGGAC TTCAGGATAA TTTGTTATCA
28501 AAAGGTCCAC CCAGCAGCTT GCTCCAAAT TTAACTCTA TCTAATCGGT
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28601 TTGTGAACTA TTTTCAAGTTT GACCAATTGT GAAATGAAATA CAAATATCTC
28651 CTAGACCCAT TCTAGTGAAGA AATGTTTGT TCTGCTTC TTAATATGTTA
28701 GATTGAGG TTTAAGTATG TGATAAAATG TAAGGCTCT TCTGGTGTAA
28751 AAATGCTGAA GTATTTATA TGTAGGTATG PACATATAAC CTTATATATG
28801 TGTGTGTTATA TTATATGTAT GCACACACAC ACACACAAAT ATGAACTTTT
28851 TGTGCAACA TCTATTAAGC TTTGGTTT GTTTGTTTA TAAATTAAGA
28901 ATCATATCAT ATATGCTATT CTTTTTAAAC CTGCTCTT TT GAACTAAAAA
28951 GATTGTAAGC ATTCTCTAGA TTATTGAATC TTTTCTTGC CTTGATTTT
29001 TAATAATCAC AGGGTATTCC ATCATCTTGG TGTACTAAAT GAAATTAACTA
29051 TTACTCCATT GTTGAACCTG TAGGTTGTAT CTCTGAAATG TATTCCTT
29101 CTTCTTCAA CTAGGATTCT AAATTGACTG ATAGGTGAGG CTTGGGCATC
29151 TGAGATATTA AGAATAATAT GGCTCAATAT ATAGATCAGA TGGGATATT
29201 ATGTAACAAA CTAAAAAACAA AATTGTAATA AGTATGGTT CTTGCTCTC
29251 AACAGAGCTC CTGTGAAATTA CAGGCTTAA TTTTCTTGT GGTGAAATA
29301 TTCTTCATGA TTGGAAGCAT GGCACCTCATT ATAATTGACT GGTATTTGTA
29351 CCCTCCAAAT TCCAAGCATC ACTAACACAA GGAAGAACAC TTTTCTTTC
29401 TATTGAAAT GGTACAAGT TATACTCCAA AAGATAATTG AATTATCTTG
29451 ATTGGAATGT TATTGATAGG AAATAACACG AAGATTTGA AGAAGTTAC
29501 CAGTAATATC ACCAGGCACC TGCAGGAAGAG GAAAATTAAT GTTTTGTCA
29551 AGGATGGTTG TGTATGTGTT TAAATAAAAA CCTCTGATGTC AGATTTCTAC
29601 CCAGGTTTG CTAGGCACT GTGAGATGAT GAAGGTAT TTTGCTGCT
29651 TTACGACCG AATAAGGTA ACTGCACTGTA ACAATCACAA GAACTACTC
29701 TTTCCCTGC CGTCTCTCA TCTGCAACCC CCTAAAGAAG TACCAAACAT
29751 TTCCATTTTC AGACATCAA ACAGAAATGC CTGCTGAAAGAATATCA
29801 CATTAAATGT CTTCTCTCA TCTGCAACCA AAGTCTTGTG TCTGTTACT
29851 AACAGAGGCA AAAGGCATGT CTTAGGAAC TTTCTCTTCTGAAAGGTA
29901 CATGAATGGT CAAACACAG TCTAGAGCAT CTTATTGTC AAGCCAAAT
29951 AATATTTGC CCACCTGTT TGTGACATTG AGITGTGACT TCTATATTC
30001 ATAGATTTT GTAAATGTTA AAACATCTAT ATTTAAATGT TAAACACTA
30051 AATATAGAGA GGGCTTAT TTCAATCATA GACCAACAC AAAATAATG
30101 CTTATAGCTA AACTGCCGT TCTAGAAAGC ATCTGCTTT TCATGTTATT
30151 CCTAAATCCT CTTGTCATAC TTTGTCATT GAACAATGTT CTCCCTCTCG
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30251 CTACCCAGTA TTGTTGATA CATTTTATT TGATAAACAT TCAGTGCAGG
30301 AAATGTTGAT TTGCTATATG TTATATGTATA TAATCTTATT CTGTTAGTCAT
30351 CAGAATGTTA ATGTAAGGT CATTGATTT TTATTTTTTA CAIGTGTAGT
30401 TTTCTTCTT CACAGCTAA GCATTTATAT TATTGGGGGT GGGGGCAGGG
30451 AATTAAGTTG GTGGGCTCGA AAATCCATTG ATATGTTATCT GTCTACAAAT
30501 GTCTGGGAT ATTTAAATT TGAAACCTAA GTTATATATA GTTGGCAAT
30551 GCTCTTCTTC AATATTACA ATAATAGGAT GATCTACAG AAAATAAGTT
30601 TCTTTTGCA AATTTTATC ATACTAAAGT TGTCTTTTA ATTTAGCATA
30651 TCTAAATAG GAATTAGTTC AGTTAGTC ACACAGGTT TTGCTGACAT
30701 TCATTGGCCA TTTAATACAG TGTGAGTGG TTCTGGTAA AAGTATAAGT
30751 GCTAACACTA CGAAGAAATG CACACGATCA TTCTGCTTA CTTCTATAAC
30801 AAACCTACAT AAAATGGATT TAAAAATTCC TACTCACAGC CTAAAACCTC
30851 TGGAGTTCAC TACCTTTTT TCAAATCATA GAAAGATCAC TTGTGTATTT
30901 TATATTTAG TAAAGCAAT TATGAAGTAC AAGTATCATA CACGTACTTT
30951 TGAGCTACTA TTATTGAAA AAAATCTGCC AAATAGCAGC TTTAGGATAT
31001 ATTTACATTT TCACTCATCT AAAAAGTATA CAAAATAAA AAGTGGAAAA
31051 AGGTATCTTC TGAATGTTCA AGAGCATCT ATAGTGCTAA ATAATAAAAGC
31101 ACCATTTTT TCTTCATAAC CAGGATTAAA ATTCAATATAT ACTGCAGGGC
31151 AGACATACAT ATGATAGCTT GTGCTGATTA ATTTAAACCC ATTTGAAAC
31201 AGATGAAAAT TTTATTTCT TATTCATTT ATAAGAAGGC TCAATGTTATT
31251 GGGAGGCTTC TTTTTTATTA CAGAAAGTGT ATATTGGTAT ATAATAAAATG
31301 AACTTTCAA ATGACTATGA TGTGATTTT GATCTATTGT TAAAGAATGT
31351 TGTGTTATTT GTCCATGAAA CAAATTTAA ATTCGAATAA CTGCTTCT
31401 TATATTGGTT TATGTTCCAT TTTCAATTGTT ACCTTTGAA CATAACTAAC
31451 ATCTATAGCC ATCATCCGAA AAATAATTGC CATCTTATTT TGGCAAAATA

FIGURE 3, page 10 of 23

31501 GATATTAAAT CCTAAATTAT TATGATGATT ATAATTTGG CATCACATAT
 31551 ATACCACCTA GAATGAATGT GGAAGAAATG AGTCTTTAT GGTAGTTG
 31601 AAAGAAATCCA TTGAAGATAG AAAATGAGAG AATAGAAGAA ACCAGAGAAAT
 31651 AGTAAAATAA AGACAGAGA AAATATGGGG GCAGGGAAAA CATGTGAGTG
 31701 CTAAGGATTG ATTATGAATG AACGATTAGG GGGATTGATG GACACAGGG
 31751 TAAGTATATG CTTAACTTTA TAAGAAAATT CCACATACTT TTGACACAGTG
 31801 TTTCATACAT TTTCATTTCC ACCCGTACTA CCTACAACCTT CCACGTGACTG
 31851 CACAGGCTG CCAACATTTG GTGTTGTCTT TTGCATTTTA GCCTTTCTAG
 31901 TGGGTCTGAA ATGCTAACG ATGTTGATTT TCATTTCTGC TTCTGTGACA
 31951 ACTAATGTTG AAAACTTTC AAGTGTAA TGGTCACTCA TATATCTCT
 32001 TTGTGAAAGT GTGTATTCAA ATCTTTGCC CATTTTAAA ATTTAGGTTA
 32051 TGTCTTTTA TTGGGTATTT GTAGAAGCTC TTTAAATATG GATCCATGTC
 32101 CAGATGGCCA ATATATTTTC CCAGTCTATG GTATGGTTGC TTATTTCT
 32151 AAAGGTGCTC TAATTACATC TTCTGGGGC CAGGTCAACCA TAGCTCAAAG
 32201 TTTTGCAATT TATGCTTAA TGAGATAATA TTAATCAGAG TGGTATAGTC
 32251 AAAATTAAAT CTTTTGATGT CCTGGGCCA TATAGGTAGG ACTGGATCAT
 32301 CTAACCAAGA TGCAAAAAAA AAAAACAAAAA AAAACAAAAA TAGTACTTGG
 32351 AAAACTTAT TTTAAATTAA ACA

FEATURES:

Start: 3000
 Exon: 3000-3118
 Intron: 3119-7453
 Exon: 7453-7543
 Intron: 7544-8039
 Exon: 8040-8155
 Intron: 8156-10824
 Exon: 10895-10968
 Intron: 10969-11107
 Exon: 11438-11530
 Intron: 11531-16047
 Exon: 16048-16129
 Intron: 16130-16215
 Exon: 16216-16298
 Intron: 16299-16408
 Exon: 16409-16467
 Intron: 16468-17301
 Exon: 17302-17577
 Intron: 17578-17709
 Exon: 17710-17789
 Intron: 17790-19073
 Exon: 19074-19174
 Intron: 19175-20904
 Exon: 20905-21029
 Intron: 21030-26649
 Exon: 26650-26794
 Intron: 26795-27670
 Exon: 27671-27763
 Intron: 27769-29273
 Exon: 29274-29372
 Stop: 29373

CHROMOSOME MAP POSITION:

Chromosome 12

ALLELIC VARIANTS (SNPs):

Position	DNA			Domain	Protein		
	Major	Minor	Position		Major	Minor	
1386	T	C		Beyond ORF(5')			
2594	T	C		Beyond ORF(5')			
2757	G	T		Beyond ORF(5')			
6107	C	T		Intron			
6392	T	C		Intron			

9484	C	G	Intron			
10330	A	G	Intron			
10397	G	A	Intron			
10331	G	A	Intron			
10536	T	C	Intron			
11448	T	C	Intron			
11917	G	T	Intron			
11840	T	-	Intron			
11844	A	-	Intron			
12847	T	-	Intron			
13019	C	-	Intron			
13022	A	G	Intron			
13285	G	A	Intron			
14461	G	C	Intron			
15464	-	G	Intron			
15469	-	A	Intron			
15545	T	C	Intron			
16199	T	C	Intron			
16798	T	C	Intron			
18103	C	T	Intron			
18421	A	G	Intron			
18538	G	A	Intron			
18722	T	C	Intron			
18775	C	G	Intron			
18951	T	C	Intron			
18974	T	G	Intron			
19540	A	C	Intron			
19641	G	A	Intron			
20170	A	C	Intron			
20343	T	C	Intron			
20519	G	A	Intron			
20963	T	C	Exon	411	P	P
21840	G	T	Intron			
22783	C	T	Intron			
22787	G	A	Intron			
22825	T	C	Intron			
22967	A	T	Intron			
23248	A	G	Intron			
23764	G	T	Intron			
23765	C	T	Intron			
24432	A	G	Intron			
24538	C	G	Intron			
24693	T	C	Intron			
24819	C	T	Intron			
25743	C	T	Intron			
26044	G	C	Intron			
26555	G	A	Intron			
27886	A	C	Intron			
31884	T	C	Beyond ORF(3')			
32229	T	A	Beyond ORF(3')			

Context:

Position	DNA
1386	ACCCATATGCAAGTCTTACTTCTATTCTCTCTAGCTTTAACCTGCTCTTTCATCTT TTATGTATATACTTTAGCTGCCCTATATAATAATAATAGTTCATTTGTTCTCCTGC TTAAAACACTGTGTGCTATTTTAAATTCTGAGAACTGCTTCTTTATTTCTAGACAA TTCTCTGCCATTATCTCTTCTGTTTGTCTCACCCTAGTCTCACAAATTCTCTATATTGG AATGACTATCAGTGTATATTGAACCTGTAATTCTTATTTTCCCCATTCTCTTAACT [T, C] CTTATTGTATTTCTTTTTAACTCTCTCATGCTATAATTGAGTGATTCCACAGA TCTGTCTTCATAAGTCTCCTCAGCTGAGTTTTAAATTCAATGATTCT

2594	<p>ATTTTTTTCTTTTTTTAAAGAATTCTTTTTTGACTCTTTTGCAACAGCCTGTCCTCC TTTATATATCTTTATAATGTTTTATTCTGTAAAGTATTCTTATTCTTATTCTTAAATTAAATGTAAGAAGCTTAAATGCTTTG CTGAACTTTCTTTGTTACTATTCTTAACTTTGGCTTCAGGATCCAAGTGCCCTAAGAAGT TACTCTTAAACTTGATCTCACCTATGTTGATATTATCAAGCATTTGGCTGCTGTTAAT TCTTCTATGTCCTAAATTAAAGCAGTAATTCTTTCTAGTTATTGCTAGTAGAGAGAC ACTGGTAGATCTGCCTGGTAGACCTCTGTCACAAATTTACTTTGTCCTGCTGTT CTTTAAAGATGTATCCACTCACAAATCTAAATTCTTGAAGACTGCTGCGATGTT [T, C] TTAAGATTTCTTTCTCATAGTGAACTGAAAAACTGCCATTTCATTATACTAG GCACTCTATAAATATCTGCTAATTAGCAATTATTAGTAATTCTTCTTCTGCTGCTG TTGCTGTTCTGTTGTTGAGGAACTTCAGGATTGCTATGTAAGTTCTA GCACTTTCTTCTCTTCTCCTTTACAGAGAGCATAAAATGTAGATGATTCTATTC ACTTATTCTATTTAAATAAAATTATAATGATGATGTTGTCAGAGAACTGAGAG 2757</p>
6107	<p>TTAFTGCTAAGAGACACTGGTAGATTCTGCCCTGGTAGACCTTCCTCTGTCACAAAT TACTTTTGTTCTCTTCTTTAAACATGATCCCACCTCACAAATACCTAAATTCTG GAGACTGCGCAGATGTTTAAGATTCTTTCTTCTCATAGTGACTGAACTAACTG CATTTTCATTATACATAGGCACTCTATAAATATCTGCTAATTAGCAATTATTAGTAATT TCTTCTTCTTCTTCTCCATTCTTCTTCTGTATTGGTAGAAAGGAAACATTCAAGGATT [G, T] CTTATGTAAGTTTCAGGAGTTCTTCTCCCTTACAGAGAGCATAAAAT GTAGATGATTCTATTCACTTATTCACTTATTCAATTAAATAATTATAATGATGATGTTGTT CTGTTTGCAAGACAGAGTGTCTGAACTCAACACAAAGTGGAGAACCTTAAGTGAAG GTACAGTATAATTACTGAGAAGGGCTGTGTGTGGACAAGAAAGCCTGACAGCTC AAATGGATCTGATGAACTGAGAAATGTCAACATCGAACAGATGATGAGAGCAGCAGTG 6392</p>
6392	<p>CTTTCTCTCTCTCTTCTATCTACATCTCATACTGTTCTCTCAAAAGTAAACCT GTCATCTCTCTCTCTCCAGATTATTTCAGGATTAGCTCTGTTATAAAAGTAGCTT GTACAGATCTCTACAAATAATTATTTCTATTCTATTCTAAGGTTTATTATTTATT TTGAGACAGACAGAGTTCACTCTGTGGCCCATGCTGGAGTGCAATGGCAATCTGG CTCACTGCAACCTCTGCCCTCCAGGTTCAAGGATTCTCTGCTTCAGCTCTGAGTAG [C, T] TGGGATATCAGGGCCTGCCACACACTGGCTAACCTTTGTTATTCTAGTAGAGAGCA AGTTTCACCATGTTGCCAGGCTGGCTTGAACTCTGACCTCAAGTTATCCACCCACCT CAGCCTCCAAAGTGTGGATTACAGGCGTGAGCCACTGTGCTGGCTCTAGGATTAT ATTAATAGAACATCTTCAATTATTATCTTCTTCTTCTTCTTCTGAGGAAAT GTCCTAAATTCTCAACCCCTCAATTGAAAGCACTTTAAATCATACATAGTCGAGCA 9484</p>
9484	<p>CAGCCTCTGAGTAGCTGGGATTACAGGCGCTGCCACACACTGGCTAACCTTTGTA TTTCTAGTAGAGACGAAGTTTCACCATGTTGCCAGGCTGGCTTGAACTCTGACCTCA AGTTATCCACCCACCTCAGCCTCCAAAGTGTGGATTACAGGCGTGAGCCACTGTG TGGCCTCTAGGATTATATAATAGAACATCTCAATTATTATCTTCTTATCTTC TTTCTATGTAAGGAAATGTCTAAATTCTCAACCCCTCAATTGAAAGCACTTTAAAT [T, C] ATACATAGTGGACGATTTATATAAAACAACTAAAGTCTGTGACATTTCAGTATA AAATGCAATGGCAGCAGCAGGCTTATTAAATTGAGCCTCTGAAATGGCTGGCTGGCT AGGTCGCTAGGCTCAAAGGCCCTGGCTTGAACTGCAAGGAGCTGACCAGCACAGCTAT AACAAAGTTGTACATCTCTAGCCTGTGTCAAGAAAACCAGAACATCACACGCTGTGG ATAGTGACATCTTAAAGTTCTTCCCTCCAACTCTTGCCTGAGTCATTGAAATTG GCAACATTATATCACAAATATGTCGTTATGTTCTGAATATCACATATGATTAGTAA TCACACAGCTATTGAGGGCTAACGATCACGGACTATAAATATTGTATTGTTAGTG TTGATTGAACTCTTCTATGATAATTCTTCAGCTGAATGGTTTTATATCACTT CTTCTATATAAGCCATGTTGAAATAAACTAGGATTTTAATATCTGAATTAAATG TATGTTGTTGTTGAACTTAAATGCAAGGAGCTGCTTACCTCTAAAGACAAAAAA [C, G] CTGCTTCTTCTTATTAATTATACATACCTTAAAGAATTAGGAAGGTTACAGATG ATGAATAGAAATAGGAAAGCTTCCCTCAACTCCACAGTCAGTCAAGATCATCTTCATGAG AAAGATGTTGCACTTTTAAATGAGGGCTCATTTAGGCTTATAAACACTTAGCAGAT GAATTGTTGAGAACAACTAAATGCAACTAACATCATGGGGTGTGTTTGTGTC AGGCCAGACTGGGATTAAGCTTCTCTTAAATTATAGCAAGTGAACACAAGTATT TTAAAG</p>

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27886 GGGTTATTAAAGTGTGCTGGCATCTCCTTGCTAGGAACGCTGGCTAAGACATTGA
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